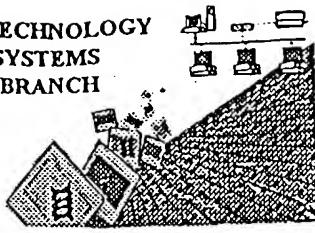# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/680,963_

Source: _1FWO_

Date Processed by STIC: _12/21/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: *10/680,963*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2 ____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ✓ Skipped Sequences (NEW RULES)
Sequence(s) *7-8* missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number ← *This is the valid format for intentionally skipped sequences.*
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa
"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 12/21/2004
PATENT APPLICATION: US/10/680,963   TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

```
 3  <110> APPLICANT: GlycoFi, Inc.
 4        Bobrowicz, Piotr
 5        Hamilton, Stephen R.
 6        Gerngross, Tilman U.
 7        Wildt, Stefan
 8        Choi, Byung-Kwon
 9        Nett, Juergen H.
10        Davidson, Robert C.
12  <120> TITLE OF INVENTION: N-Acetylglucosaminyltransferase III expression in lower
13        eukaryotes
15  <130> FILE REFERENCE: GFI-108 CIP
17  <140> CURRENT APPLICATION NUMBER: US 10/680,963
18  <141> CURRENT FILING DATE: 2003-10-07
20  <150> PRIOR APPLICATION NUMBER: US 10/371,877
21  <151> PRIOR FILING DATE: 2003-02-20
23  <150> PRIOR APPLICATION NUMBER: US 09/892,591
24  <151> PRIOR FILING DATE: 2001-06-27
26  <150> PRIOR APPLICATION NUMBER: US 60/214,358
27  <151> PRIOR FILING DATE: 2000-06-28
29  <150> PRIOR APPLICATION NUMBER: US 60/215,638
30  <151> PRIOR FILING DATE: 2000-06-30
32  <150> PRIOR APPLICATION NUMBER: US 60/279,997
33  <151> PRIOR FILING DATE: 2001-03-30
35  <150> PRIOR APPLICATION NUMBER: PCT/US02/41510
36  <151> PRIOR FILING DATE: 2002-12-24
38  <150> PRIOR APPLICATION NUMBER: US 60/344,169
39  <151> PRIOR FILING DATE: 2001-12-27
41  <160> NUMBER OF SEQ ID NOS: 101
43  <170> SOFTWARE: PatentIn version 3.2
45  <210> SEQ ID NO: 1
46  <211> LENGTH: 3
47  <212> TYPE: PRT
48  <213> ORGANISM: artificial
50  <220> FEATURE:
51  <223> OTHER INFORMATION: Glycosylation target
54  <220> FEATURE:
55  <221> NAME/KEY: MISC_FEATURE
56  <222> LOCATION: (2)..(2)
57  <223> OTHER INFORMATION: wherein "Xaa" is any amino acid except proline
59  <400> SEQUENCE: 1
61  Asn Xaa Ser
62  1
65  <210> SEQ ID NO: 2
```

pp 1-3, 6

Does Not Comply
Corrected Diskette Needed

give source of genetic material
(see item 11 on Error Summary
Sheet)

W-->

RAW SEQUENCE LISTING   DATE: 12/21/2004
PATENT APPLICATION: US/10/680,963   TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

```
 66 <211> LENGTH: 3
 67 <212> TYPE: PRT
 68 <213> ORGANISM: artificial
 70 <220> FEATURE:
 71 <223> OTHER INFORMATION: Glycosylation target        same error
 74 <220> FEATURE:
 75 <221> NAME/KEY: MISC_FEATURE
 76 <222> LOCATION: (2)..(2)
 77 <223> OTHER INFORMATION: wherein "Xaa" is any amino acid except proline
 79 <400> SEQUENCE: 2
```
W--> 81 Asn Xaa Thr
```
 82 1
 85 <210> SEQ ID NO: 3
 86 <211> LENGTH: 21
 87 <212> TYPE: DNA
 88 <213> ORGANISM: artificial
 90 <220> FEATURE:
 91 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,6-
mannosyltransferase)
 93 <400> SEQUENCE: 3
 94 atggcgaagg cagatggcag t                                          21
 97 <210> SEQ ID NO: 4
 98 <211> LENGTH: 21
 99 <212> TYPE: DNA
100 <213> ORGANISM: artificial
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,6-
mannosyltransferase)
105 <400> SEQUENCE: 4
106 ttagtccttc caacttcctt c                                          21
109 <210> SEQ ID NO: 5
110 <211> LENGTH: 26
111 <212> TYPE: DNA
112 <213> ORGANISM: artificial
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,2
116         mannosyltransferases)
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (9)..(9)
122 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
124 <220> FEATURE:
125 <221> NAME/KEY: misc_feature
126 <222> LOCATION: (12)..(12)
127 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
129 <220> FEATURE:
130 <221> NAME/KEY: misc_feature
131 <222> LOCATION: (18)..(18)
132 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
134 <400> SEQUENCE: 5
```
W--> 135 taytggmgng tngarcynga yathaa   26

RAW SEQUENCE LISTING　　　　　　　　DATE: 12/21/2004
PATENT APPLICATION:　US/10/680,963　　TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

```
138 <210> SEQ ID NO: 6
139 <211> LENGTH: 20
140 <212> TYPE: DNA
141 <213> ORGANISM: artificial
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,2
145       mannosyltransferases)
148 <220> FEATURE:
149 <221> NAME/KEY: misc_feature
150 <222> LOCATION: (6)..(6)
151 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
153 <220> FEATURE:
154 <221> NAME/KEY: misc_feature
155 <222> LOCATION: (12)..(12)
156 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
158 <400> SEQUENCE: 6
```

W--> 159 gcrtcncccc anckytcrta　　　　　　　　　　　　　　　　　20

```
162 <210> SEQ ID NO: 7
163 <211> LENGTH: 0
164 <212> TYPE: DNA
165 <213> ORGANISM: Kluyveromyces lactis
167 <400> SEQUENCE: 7
```

delete this section (see item 8 on Error summary sheet) for valid format

W--> 168 000

```
170 <210> SEQ ID NO: 8
171 <211> LENGTH: 0
172 <212> TYPE: PRT
173 <213> ORGANISM: Kluyveromyces lactis
175 <400> SEQUENCE: 8
```

delete

Do the same with Sequences 43 and 44

W--> 176 000

```
178 <210> SEQ ID NO: 9
179 <211> LENGTH: 458
180 <212> TYPE: PRT
181 <213> ORGANISM: Saccharomyces cerevisiae
184 <220> FEATURE:
185 <221> NAME/KEY: MISC_FEATURE
186 <222> LOCATION: (304)..(318)
187 <223> OTHER INFORMATION: Low-complexity sequence
189 <220> FEATURE:
190 <221> NAME/KEY: MISC_FEATURE
191 <222> LOCATION: (416)..(436)
192 <223> OTHER INFORMATION: Low-complexity sequence
194 <400> SEQUENCE: 9
```

yes, but which amino acid(s) do the Xaa's represent?

same error

```
196 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
197 1                   5                   10                  15
200 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
201             20                  25                  30
204 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
205         35                  40                  45
208 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
```

```
209       50                      55                      60
212 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
213 65                      70                      75                      80
216 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
217                     85                      90                      95
220 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
221                     100                     105                     110
224 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
225                 115                     120                     125
228 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
229             130                     135                     140
232 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
233 145                     150                     155                     160
236 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
237                 165                     170                     175
240 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
241                 180                     185                     190
244 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
245             195                     200                     205
248 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
249 210                     215                     220
252 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
253 225                     230                     235                     240
256 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
257                 245                     250                     255
260 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
261             260                     265                     270
264 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
265             275                     280                     285
268 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa
269         290                     295                     300
272 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Val
273 305                     310                     315                     320
276 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
277                 325                     330                     335
280 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
281             340                     345                     350
284 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
285             355                     360                     365
288 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
289         370                     375                     380
292 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
293 385                     390                     395                     400
296 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Xaa
297             405                     410                     415
300 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
301             420                     425                     430
304 Xaa Xaa Xaa Xaa Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
305             435                     440                     445
```

W--> (at line 268)

```
308 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
309     450                 455
312 <210> SEQ ID NO: 10
313 <211> LENGTH: 458
314 <212> TYPE: PRT
315 <213> ORGANISM: Saccharomyces cerevisiae
317 <400> SEQUENCE: 10
319 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
320 1               5                   10                  15
323 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
324             20                  25                  30
327 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
328             35                  40                  45
331 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
332     50                  55                  60
335 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
336 65                  70                  75                  80
339 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
340                 85                  90                  95
343 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
344             100                 105                 110
347 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
348             115                 120                 125
351 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
352     130                 135                 140
355 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
356 145                 150                 155                 160
359 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
360                 165                 170                 175
363 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
364             180                 185                 190
367 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
368             195                 200                 205
371 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
372     210                 215                 220
375 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
376 225                 230                 235                 240
379 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
380             245                 250                 255
383 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
384             260                 265                 270
387 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
388             275                 280                 285
391 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
392     290                 295                 300
395 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
396 305                 310                 315                 320
399 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
400             325                 330                 335
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/21/2004
PATENT APPLICATION: **US/10/680,963** TIME: 11:33:41

Input Set : **A:\GFI-108 Sequence listing.ST25.txt**
Output Set: **N:\CRF4\12212004\J680963.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2
Seq#:2; Xaa Pos. 2
Seq#:5; N Pos. 9,12,18
Seq#:6; N Pos. 6,12
Seq#:9; Xaa Pos. 304,305,306,307,308,309,310,311,312,313,314,315,316,317
Seq#:9; Xaa Pos. 318,416,417,418,419,420,421,422,423,424,425,426,427,428
Seq#:9; Xaa Pos. 429,430,431,432,433,434,435,436
Seq#:11; Xaa Pos. 279,280,281,282,283,284,285,286,287,288,289,290,291,292
Seq#:11; Xaa Pos. 293
Seq#:25; Xaa Pos. 209,210,211,212,213,214,215,216,217,218,219,220,221,222
Seq#:25; Xaa Pos. 223,235,236,237,238,239,240,241,242,243,244,245,246
Seq#:27; Xaa Pos. 183,184,185,186,187,188,189,190,191,192,193,194,195,196
Seq#:27; Xaa Pos. 197,209,210,211,212,213,214,215,216,217,218,219,220
Seq#:29; Xaa Pos. 176,177,178,179,180,181,182,183,184,185,186,187,188,189
Seq#:29; Xaa Pos. 190,202,203,204,205,206,207,208,209,210,211,212,213
Seq#:31; Xaa Pos. 176,177,178,179,180,181,182,183,184,185,186,187,188,189
Seq#:31; Xaa Pos. 190,202,203,204,205,206,207,208,209,210,211,212,213
Seq#:75; N Pos. 17,20

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,41,42,47,48,49,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66
Seq#:67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,94
Seq#:95,96,97,98,99,100,101

VERIFICATION SUMMARY   DATE: 12/21/2004
PATENT APPLICATION: **US/10/680,963**   TIME: 11:33:41

Input Set : **A:\GFI-108 Sequence listing.ST25.txt**
Output Set: **N:\CRF4\12212004\J680963.raw**

```
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:168 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:176 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:288
M:341 Repeated in SeqNo=9
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:272
M:341 Repeated in SeqNo=11
L:1467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:208
M:341 Repeated in SeqNo=25
L:1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:176
M:341 Repeated in SeqNo=27
L:1909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:160
M:341 Repeated in SeqNo=29
L:2126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:160
M:341 Repeated in SeqNo=31
L:2547 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:
L:2555 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:3343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0
```